

Applicants: Short et al.
Application No.: 09/975,036
Filed: October 10, 2001
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In the Claims:

Please cancel claims 27, 29-32, 34-40 and 212-215 without prejudice.

Please amend claims 1-3, 11-14, 17, 19-21, 41, 43, and 44 as follows:

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims

1. (Currently Amended) A method for identifying in a liquid phase, a naturally occurring genomic DNA polynucleotide that directs the synthesis of a biomolecule having an activity of interest in a host cell comprising:
 - a) contacting in a liquid phase a plurality of naturally occurring genomic DNA polynucleotides obtained in a) derived from one or more organisms at least one organism with at least one nucleic acid probe that comprises a DNA sequence complementary to that directs the synthesis of a bioactivity or biomolecule of interest under conditions that allow hybridization of the probe to the genomic DNA polynucleotides having sequences of interest; and
 - b) identifying a naturally occurring polynucleotide genomic DNA that directs the synthesis of a biomolecule having an activity of interest in a host cell with an analyzer that detects a polynucleotide DNA to which a probe has hybridized.
2. (Currently Amended) The method of claim 1, wherein the polynucleotides are genomic DNA is from a mixed population of cells.
3. (Currently Amended) The method of claim 1, wherein the polynucleotides are genomic DNA is in a library.
4. (Original) The method of claim 3 wherein the library is an expression library.
5. (Original) The method of claim 3 wherein the library is an environmental expression library.

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6. (Original) The method of claim 1, wherein the nucleic acid probe is from at least about 15 bases to about 100 bases.
7. (Original) The method of claim 1, wherein the nucleic acid probe is from at least about 100 bases to about 500 bases.
8. (Original) The method of claim 1, wherein the nucleic acid probe is from at least about 500 bases to about 1,000 bases.
9. (Original) The method of claim 1, wherein the nucleic acid probe is from at least about 1,000 bases to about 5,000 bases.
10. (Original) The method of claim 1, wherein the nucleic acid probe is from at least about 5,000 bases to about 10,000 bases.
11. (Currently Amended) The method of claim 1, wherein the probe is labeled with a fluorescent molecule and the detecting involves detecting fluorescence from the fluorescent molecule ~~from a polynucleotide to which the probe has hybridized.~~
12. (Currently Amended) The method of claim 1, wherein the probe is labeled with a magnetic molecule and the detecting involves detecting a magnetic field ~~of a polynucleotide to which the probe has hybridized.~~
13. (Currently Amended) The method of claim ~~[[1]]~~12, wherein the hybridization modulates a magnetic field and the analyzer detects modulation of the magnetic field.
14. (Currently Amended) The method of claim 1, wherein the hybridization modulates the dielectric signature of ~~the the polynucleotide~~ DNA to which a probe has hybridized

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15. (Original) The method of claim 1, wherein the analyzer is a FACS analyzer.
16. (Original) The method of claim 1, wherein the analyzer is a magnetic field sensing device.
17. (Currently Amended) The method of claim ~~[[9]]~~16, wherein the magnetic field sensing device is a Super Conducting Quantum Interference Device.
18. (Original) The method of claim 1, wherein the analyzer is a multipole coupling spectroscopy device.
19. (Currently Amended) The method of claim 1, wherein the ~~organism is~~ organisms are from an environmental sample.
20. (Currently Amended) The method of claim ~~[[1]]~~19, wherein the environmental sample is selected from the group consisting of geothermal fields, hydrothermal fields, acidic soils, sulfotara mud pots, boiling mud pots, pools, hot-springs, geysers, marine actinomycetes, metazoan, endosymbionts, ectosymbionts, tropical soil, temperate soil, arid soil, compost piles, manure piles, marine sediments, freshwater sediments, water concentrates, hypersaline sea ice, super-cooled sea ice, arctic tundra, Sargosso sea, open ocean pelagic, marine snow, microbial mats, whale falls, springs, hydrothermal vents, insect and nematode gut microbial communities, plant endophytes, epiphytic water samples, industrial sites and ex situ enrichments.
21. (Currently Amended) The method of claim ~~[[2]]~~20, wherein the environmental sample is selected from the group consisting of eukaryotes, prokaryotes, myxobacteria, air, water, sediment, soil or rock.

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22. (Original) The method of claim 1, wherein the organism comprises a microorganism.
23. (Original) The method of claim 19, wherein the environmental sample contains extremophiles.
24. (Original) The method of claim 23, wherein the extremophiles are selected from the group consisting of hyperthermophiles, psychrophiles, halophiles, psychrotrophs, alkalophiles, and acidophiles.

Claims 25-40 (Cancelled)

41. (Currently Amended) The method of claim 1, wherein the DNA polynucleotide of interest encodes an enzyme.
42. (Original) The method of claim 41, wherein the enzyme is selected from the group consisting of lipases, esterases, proteases, glycosidases, glycosyl transferases, phosphatases, kinases, mono- and dioxygenases, haloperoxidases, lignin peroxidases, diarylpropane peroxidases, epoxide hydrolases, nitrile hydratases, nitrilases, transaminases, amidases, and acylases.
43. (Currently Amended) The method of claim 1, wherein the polynucleotide of interest encodes the biomolecule is a small molecule.
44. (Currently Amended) The method of claim 1, wherein the DNA polynucleotide of interest, or fragments thereof, comprise one or more operons, or portions thereof.

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45. (Original) The method of claim 44, wherein the operons, or portions thereof, encodes a complete or partial metabolic pathway.

46. (Original) The method of claim 44, wherein the operons or portions thereof encoding a complete or partial metabolic pathway encodes polyketide syntheses.

Claims 47-216 (Cancelled)